

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: US/09/983,025B

Source: IFW/6

Date Processed by STIC: 1-11-05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 01/11/2005

PATENT APPLICATION: US/09/983,025B

TIME: 16:59:07

Input Set : A:\sequence\_listing.txt

Output Set: N:\CRF4\01112005\I983025B.raw

3 <110> APPLICANT: OXVIG, Claus  
 4 OVERGAARD, Michael T.  
 6 <120> TITLE OF INVENTION: PREGNANCY-ASSOCIATED PLASMA PROTEIN-A2 (PAPP-A2)  
 8 <130> FILE REFERENCE: OXVIG=1A  
 10 <140> CURRENT APPLICATION NUMBER: US 09/983,025B  
 11 <141> CURRENT FILING DATE: 2001-10-22  
 13 <150> PRIOR APPLICATION NUMBER: US 60/241,840  
 14 <151> PRIOR FILING DATE: 2000-10-20  
 16 <150> PRIOR APPLICATION NUMBER: DK PA 2000 01571  
 17 <151> PRIOR FILING DATE: 2000-10-20  
 19 <160> NUMBER OF SEQ ID NOS: 26  
 21 <170> SOFTWARE: PatentIn version 3.3  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 8527  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Homo sapiens  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (1)..(5373)  
 32 <223> OTHER INFORMATION: prepro-PAPP-A2 coding sequence  
 34 <220> FEATURE:  
 35 <221> NAME/KEY: misc\_feature  
 36 <222> LOCATION: (1)..(66)  
 37 <223> OTHER INFORMATION: Signal peptide  
 39 <220> FEATURE:  
 40 <221> NAME/KEY: misc\_feature  
 41 <222> LOCATION: (1)..(66)  
 42 <223> OTHER INFORMATION: prepro part of PAPP-A2  
 44 <220> FEATURE:  
 45 <221> NAME/KEY: misc\_feature  
 46 <222> LOCATION: (67)..(699)  
 47 <223> OTHER INFORMATION: pro part of PAPP-A2  
 49 <220> FEATURE:  
 50 <221> NAME/KEY: misc\_feature  
 51 <222> LOCATION: (700)..()  
 52 <223> OTHER INFORMATION: Mature peptide  
 54 <220> FEATURE:  
 55 <221> NAME/KEY: 3'UTR  
 56 <222> LOCATION: (5377)..(8527)  
 58 <400> SEQUENCE: 1  
 59 atg atg tgc tta aag atc cta aga ata agc ctg gcg att ttg gct ggg 48  
 60 Met Met Cys Leu Lys Ile Leu Arg Ile Ser Leu Ala Ile Leu Ala Gly  
 61 1 5 10 15

(pg. 6)

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63	tgg gca ctc tgt tct gcc aac tct gag ctg ggc tgg aca cgc aag aaa	96
64	Trp Ala Leu Cys Ser Ala Asn Ser Glu Leu Gly Trp Thr Arg Lys Lys	
65	20 25 30	
67	tcc ttg gtt gag agg gaa cac ctg aat cag gtg ctg ttg gaa gga gaa	144
68	Ser Leu Val Glu Arg Glu His Leu Asn Gln Val Leu Leu Glu Gly Glu	
69	35 40 45	
71	cgt tgt tgg ctg ggg gcc aag gtt cga aga ccc aga gct tct cca cag	192
72	Arg Cys Trp Leu Gly Ala Lys Val Arg Arg Pro Arg Ala Ser Pro Gln	
73	50 55 60	
75	cat cac ctc ttt gga gtc tac ccc agc agg gct ggg aac tac cta agg	240
76	His His Leu Phe Gly Val Tyr Pro Ser Arg Ala Gly Asn Tyr Leu Arg	
77	65 70 75 80	
79	ccc tac ccc gtg ggg gag caa gaa atc cat cat aca gga cgc agc aaa	288
80	Pro Tyr Pro Val Gly Glu Gln Glu Ile His His Thr Gly Arg Ser Lys	
81	85 90 95	
83	cca gac act gaa gga aat gct gtg agc ctt gtt ccc cca gac ctg act	336
84	Pro Asp Thr Glu Gly Asn Ala Val Ser Leu Val Pro Pro Asp Leu Thr	
85	100 105 110	
87	gaa aat cca gca gga ctg agg ggt gca gtt gaa gag ccg gct gcc cca	384
88	Glu Asn Pro Ala Gly Leu Arg Gly Ala Val Glu Glu Pro Ala Ala Pro	
89	115 120 125	
91	tgg gta ggg gat agt cct att ggg caa tct gag ctg ctg gga gat gat	432
92	Trp Val Gly Asp Ser Pro Ile Gly Gln Ser Glu Leu Leu Gly Asp Asp	
93	130 135 140	
95	gac gct tat ctc ggc aat caa aga tcc aag gag tct cta ggt gag gcc	480
96	Asp Ala Tyr Leu Gly Asn Gln Arg Ser Lys Glu Ser Leu Gly Glu Ala	
97	145 150 155 160	
99	ggg att cag aaa ggc tca gcc atg gct gcc act act acc acc gcc att	528
100	Gly Ile Gln Lys Gly Ser Ala Met Ala Ala Thr Thr Thr Thr Ala Ile	
101	165 170 175	
103	ttc aca acc ctg aac gaa ccc aaa cca gag acc caa agg agg ggc tgg	576
104	Phe Thr Thr Leu Asn Glu Pro Lys Pro Glu Thr Gln Arg Arg Gly Trp	
105	180 185 190	
107	gcc aag tcc agg cag cgt cgc caa gtg tgg aag agg cgg gcg gaa gat	624
108	Ala Lys Ser Arg Gln Arg Arg Gln Val Trp Lys Arg Arg Ala Glu Asp	
109	195 200 205	
111	ggg cag gga gac tcc ggt atc tct tca cat ttc caa cct tgg ccc aag	672
112	Gly Gln Gly Asp Ser Gly Ile Ser Ser His Phe Gln Pro Trp Pro Lys	
113	210 215 220	
115	cat tcc ctt aaa cac agg gtc aaa aag agt cca ccg gag gaa agc aac	720
116	His Ser Leu Lys His Arg Val Lys Lys Ser Pro Pro Glu Glu Ser Asn	
117	225 230 235 240	
119	caa aat ggt gga gag ggc tcc tac cga gaa gca gag acc ttt aac tcc	768
120	Gln Asn Gly Gly Glu Gly Ser Tyr Arg Glu Ala Glu Thr Phe Asn Ser	
121	245 250 255	
123	caa gta gga ctg ccc atc tta tac ttc tct ggg agg cgg gag cgg ctg	816
124	Gln Val Gly Leu Pro Ile Leu Tyr Phe Ser Gly Arg Arg Glu Arg Leu	
125	260 265 270	
127	ctg ctg cgt cca gaa gtg ctg gct gag att ccc cgg gag gcg ttc aca	864

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128	Leu	Leu	Arg	Pro	Glu	Val	Leu	Ala	Glu	Ile	Pro	Arg	Glu	Ala	Phe	Thr	
129			275					280					285				
131	gtg	gaa	gcc	tgg	gtt	aaa	ccg	gag	gga	gga	cag	aac	aac	cca	gcc	atc	912
132	Val	Glu	Ala	Trp	Val	Lys	Pro	Glu	Gly	Gly	Gln	Asn	Asn	Pro	Ala	Ile	
133		290					295					300					
135	atc	gca	ggt	gtg	ttt	gat	aac	tgc	tcc	cac	act	gtc	agt	gac	aaa	ggc	960
136	Ile	Ala	Gly	Val	Phe	Asp	Asn	Cys	Ser	His	Thr	Val	Ser	Asp	Lys	Gly	
137	305					310					315					320	
139	tgg	gcc	ctg	ggg	atc	cgc	tca	ggg	aag	gac	aag	gga	aag	cgg	gat	gct	1008
140	Trp	Ala	Leu	Gly	Ile	Arg	Ser	Gly	Lys	Asp	Lys	Gly	Lys	Arg	Asp	Ala	
141					325					330					335		
143	cgc	ttc	ttc	ttc	tcc	ctc	tgc	acc	gac	cgc	gtg	aag	aaa	gcc	acc	atc	1056
144	Arg	Phe	Phe	Phe	Ser	Leu	Cys	Thr	Asp	Arg	Val	Lys	Lys	Ala	Thr	Ile	
145				340				345						350			
147	ttg	att	agc	cac	agt	cgc	tac	caa	cca	ggc	aca	tgg	acc	cat	gtg	gca	1104
148	Leu	Ile	Ser	His	Ser	Arg	Tyr	Gln	Pro	Gly	Thr	Trp	Thr	His	Val	Ala	
149			355					360					365				
151	gcc	act	tac	gat	gga	cgg	cac	atg	gcc	ctg	tat	gtg	gat	ggc	act	cag	1152
152	Ala	Thr	Tyr	Asp	Gly	Arg	His	Met	Ala	Leu	Tyr	Val	Asp	Gly	Thr	Gln	
153		370					375					380					
155	gtg	gct	agc	agt	cta	gac	cag	tct	ggt	ccc	ctg	aac	agc	ccc	ttc	atg	1200
156	Val	Ala	Ser	Ser	Leu	Asp	Gln	Ser	Gly	Pro	Leu	Asn	Ser	Pro	Phe	Met	
157	385					390				395						400	
159	gca	tct	tgc	cgc	tct	ttg	ctc	ctg	ggg	gga	gac	agc	tct	gag	gat	ggg	1248
160	Ala	Ser	Cys	Arg	Ser	Leu	Leu	Leu	Gly	Gly	Asp	Ser	Ser	Glu	Asp	Gly	
161				405				410						415			
163	cac	tat	ttc	cgt	gga	cac	ctg	ggc	aca	ctg	ggt	ttc	tgg	tcg	acc	gcc	1296
164	His	Tyr	Phe	Arg	Gly	His	Leu	Gly	Thr	Leu	Val	Phe	Trp	Ser	Thr	Ala	
165				420				425						430			
167	ctg	cca	caa	agc	cat	ttt	cag	cac	agt	tct	cag	cat	tca	agt	ggg	gag	1344
168	Leu	Pro	Gln	Ser	His	Phe	Gln	His	Ser	Ser	Gln	His	Ser	Ser	Gly	Glu	
169			435				440						445				
171	gag	gaa	gcg	act	gac	ttg	gtc	ctg	aca	gcg	agc	ttt	gag	cct	gtg	aac	1392
172	Glu	Glu	Ala	Thr	Asp	Leu	Val	Leu	Thr	Ala	Ser	Phe	Glu	Pro	Val	Asn	
173		450					455					460					
175	aca	gag	tgg	gtt	ccc	ttt	aga	gat	gag	aag	tac	cca	cga	ctt	gag	gtt	1440
176	Thr	Glu	Trp	Val	Pro	Phe	Arg	Asp	Glu	Lys	Tyr	Pro	Arg	Leu	Glu	Val	
177	465					470				475						480	
179	ctc	cag	ggc	ttt	gag	cca	gag	cct	gag	att	ctg	tcg	cct	ttg	cag	ccc	1488
180	Leu	Gln	Gly	Phe	Glu	Pro	Glu	Pro	Glu	Ile	Leu	Ser	Pro	Leu	Gln	Pro	
181				485				490						495			
183	cca	ctc	tgt	ggg	caa	aca	gtc	tgt	gac	aat	gtg	gaa	ttg	atc	tcc	cag	1536
184	Pro	Leu	Cys	Gly	Gln	Thr	Val	Cys	Asp	Asn	Val	Glu	Leu	Ile	Ser	Gln	
185				500				505						510			
187	tac	aat	gga	tac	tgg	ccc	ctt	cgg	gga	gag	aag	gtg	ata	cgc	tac	cag	1584
188	Tyr	Asn	Gly	Tyr	Trp	Pro	Leu	Arg	Gly	Glu	Lys	Val	Ile	Arg	Tyr	Gln	
189			515					520					525				
191	gtg	gtg	aac	atc	tgt	gat	gat	gag	ggc	cta	aac	ccc	att	gtg	agt	gag	1632
192	Val	Val	Asn	Ile	Cys	Asp	Asp	Glu	Gly	Leu	Asn	Pro	Ile	Val	Ser	Glu	

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193	530	535	540	
195	gag cag att cgt ctg cag cac gag gca ctg aat gag gcc ttc agc cgc	1680		
196	Glu Gln Ile Arg Leu Gln His Glu Ala Leu Asn Glu Ala Phe Ser Arg			
197	545 550 555 560			
199	tac aac atc agc tgg cag ctg agc gtc cac cag gtc cac aat tcc acc	1728		
200	Tyr Asn Ile Ser Trp Gln Leu Ser Val His Gln Val His Asn Ser Thr			
201	565 570 575			
203	ctg cga cac cgg gtt gtg ctt gtg aac tgt gag ccc agc aag att ggc	1776		
204	Leu Arg His Arg Val Val Leu Val Asn Cys Glu Pro Ser Lys Ile Gly			
205	580 585 590			
207	aat gac cat tgt gac ccc gag tgt gag cac cca ctc aca ggc tat gat	1824		
208	Asn Asp His Cys Asp Pro Glu Cys Glu His Pro Leu Thr Gly Tyr Asp			
209	595 600 605			
211	ggg ggt gac tgc cgc ctg cag ggc cgc tgc tac tcc tgg aac cgc agg	1872		
212	Gly Gly Asp Cys Arg Leu Gln Gly Arg Cys Tyr Ser Trp Asn Arg Arg			
213	610 615 620			
215	gat ggg ctc tgt cac gtg gag tgt aac aac atg ctg aac gac ttt gac	1920		
216	Asp Gly Leu Cys His Val Glu Cys Asn Asn Met Leu Asn Asp Phe Asp			
217	625 630 635 640			
219	gac gga gac tgc tgc gac ccc cag gtg gct gat gtg cgc aag acc tgc	1968		
220	Asp Gly Asp Cys Cys Asp Pro Gln Val Ala Asp Val Arg Lys Thr Cys			
221	645 650 655			
223	ttt gac cct gac tca ccc aag agg gca tac atg agt gtg aag gag ctg	2016		
224	Phe Asp Pro Asp Ser Pro Lys Arg Ala Tyr Met Ser Val Lys Glu Leu			
225	660 665 670			
227	aag gag gcc ctg cag ctg aac agt act cac ttc ctc aac atc tac ttt	2064		
228	Lys Glu Ala Leu Gln Leu Asn Ser Thr His Phe Leu Asn Ile Tyr Phe			
229	675 680 685			
231	gcc agc tca gtg cgg gaa gac ctt gca ggt gct gcc acc tgg cct tgg	2112		
232	Ala Ser Ser Val Arg Glu Asp Leu Ala Gly Ala Ala Thr Trp Pro Trp			
233	690 695 700			
235	gac aag gac gct gtc act cac ctg ggt ggc att gtc ctc agc cca gca	2160		
236	Asp Lys Asp Ala Val Thr His Leu Gly Gly Ile Val Leu Ser Pro Ala			
237	705 710 715 720			
239	tat tat ggg atg cct ggc cac acc gac acc atg atc cat gaa gtg gga	2208		
240	Tyr Tyr Gly Met Pro Gly His Thr Asp Thr Met Ile His Glu Val Gly			
241	725 730 735			
243	cat gtt ctg gga ctc tac cat gtc ttt aaa gga gtc agt gaa aga gaa	2256		
244	His Val Leu Gly Leu Tyr His Val Phe Lys Gly Val Ser Glu Arg Glu			
245	740 745 750			
247	tcc tgc aat gac ccc tgc aag gag aca gtg cca tcc atg gaa acg gga	2304		
248	Ser Cys Asn Asp Pro Cys Lys Glu Thr Val Pro Ser Met Glu Thr Gly			
249	755 760 765			
251	gac ctc tgt gcc gac acc gcc ccc act ccc aag agt gag ctg tgc cgg	2352		
252	Asp Leu Cys Ala Asp Thr Ala Pro Thr Pro Lys Ser Glu Leu Cys Arg			
253	770 775 780			
255	gaa cca gag ccc act agt gac acc tgt ggc ttc act cgc ttc cca ggg	2400		
256	Glu Pro Glu Pro Thr Ser Asp Thr Cys Gly Phe Thr Arg Phe Pro Gly			
257	785 790 795 800			

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259	gct	ccg	ttc	acc	aac	tac	atg	agc	tac	acg	gat	gat	aac	tgc	act	gac	2448
260	Ala	Pro	Phe	Thr	Asn	Tyr	Met	Ser	Tyr	Thr	Asp	Asp	Asn	Cys	Thr	Asp	
261					805					810					815		
263	aac	ttc	act	cct	aac	caa	gtg	gcc	cga	atg	cat	tgc	tat	ttg	gac	cta	2496
264	Asn	Phe	Thr	Pro	Asn	Gln	Val	Ala	Arg	Met	His	Cys	Tyr	Leu	Asp	Leu	
265				820					825					830			
267	gtc	tat	cag	cag	tgg	act	gaa	agc	aga	aag	ccc	acc	ccc	atc	ccc	att	2544
268	Val	Tyr	Gln	Gln	Trp	Thr	Glu	Ser	Arg	Lys	Pro	Thr	Pro	Ile	Pro	Ile	
269			835					840					845				
271	cca	cct	atg	gtc	atc	gga	cag	acc	aac	aag	tcc	ctc	act	atc	cac	tgg	2592
272	Pro	Pro	Met	Val	Ile	Gly	Gln	Thr	Asn	Lys	Ser	Leu	Thr	Ile	His	Trp	
273		850					855				860						
275	ctg	cct	cct	att	agt	gga	gtt	gta	tat	gac	agg	gcc	tca	ggc	agc	ttg	2640
276	Leu	Pro	Pro	Ile	Ser	Gly	Val	Val	Tyr	Asp	Arg	Ala	Ser	Gly	Ser	Leu	
277	865				870				875				880				
279	tgt	ggc	gct	tgc	act	gaa	gat	ggg	acc	ttt	cgt	cag	tat	gtg	cac	aca	2688
280	Cys	Gly	Ala	Cys	Thr	Glu	Asp	Gly	Thr	Phe	Arg	Gln	Tyr	Val	His	Thr	
281				885					890				895				
283	gct	tcc	tcc	cgg	cgg	gtg	tgt	gac	tcc	tca	ggt	tat	tgg	acc	cca	gag	2736
284	Ala	Ser	Ser	Arg	Arg	Val	Cys	Asp	Ser	Ser	Gly	Tyr	Trp	Thr	Pro	Glu	
285			900					905				910					
287	gag	gct	gtg	ggg	cct	cct	gat	gtg	gat	cag	ccc	tgc	gag	cca	agc	tta	2784
288	Glu	Ala	Val	Gly	Pro	Pro	Asp	Val	Asp	Gln	Pro	Cys	Glu	Pro	Ser	Leu	
289			915				920				925						
291	cag	gcc	tgg	agc	cct	gag	gtc	cac	ctg	tac	cac	atg	aac	atg	acg	gtc	2832
292	Gln	Ala	Trp	Ser	Pro	Glu	Val	His	Leu	Tyr	His	Met	Asn	Met	Thr	Val	
293		930				935			940								
295	ccc	tgc	ccc	aca	gaa	ggc	tgt	agc	ttg	gag	ctg	ctc	ttc	caa	cac	ccg	2880
296	Pro	Cys	Pro	Thr	Glu	Gly	Cys	Ser	Leu	Glu	Leu	Leu	Phe	Gln	His	Pro	
297	945				950			955				960					
299	gtc	caa	gcc	gac	acc	ctc	acc	ctg	tgg	gtc	act	tcc	ttc	ttc	atg	gag	2928
300	Val	Gln	Ala	Asp	Thr	Leu	Thr	Leu	Trp	Val	Thr	Ser	Phe	Phe	Met	Glu	
301				965				970				975					
303	tcc	tcg	cag	gtc	ctc	ttt	gac	aca	gag	atc	ttg	ctg	gaa	aac	aag	gag	2976
304	Ser	Ser	Gln	Val	Leu	Phe	Asp	Thr	Glu	Ile	Leu	Leu	Glu	Asn	Lys	Glu	
305			980				985				990						
307	tca	gtg	cac	ctg	ggc	ccc	tta	gac	act	ttc	tgt	gac	atc	cca	ctc	acc	3024
308	Ser	Val	His	Leu	Gly	Pro	Leu	Asp	Thr	Phe	Cys	Asp	Ile	Pro	Leu	Thr	
309			995				1000				1005						
311	atc	aaa	ctg	cac	gtg	gat	ggg	aag	gtg	tcg	ggg	gtg	aaa	gtc	tac		3069
312	Ile	Lys	Leu	His	Val	Asp	Gly	Lys	Val	Ser	Gly	Val	Lys	Val	Tyr		
313		1010				1015			1020								
315	acc	ttt	gat	gag	agg	ata	gag	att	gat	gca	gca	ctc	ctg	act	tct		3114
316	Thr	Phe	Asp	Glu	Arg	Ile	Glu	Ile	Asp	Ala	Ala	Leu	Leu	Thr	Ser		
317		1025				1030			1035								
319	cag	ccc	cac	agt	ccc	ttg	tgc	tct	ggc	tgc	agg	cct	gtg	agg	tac		3159
320	Gln	Pro	His	Ser	Pro	Leu	Cys	Ser	Gly	Cys	Arg	Pro	Val	Arg	Tyr		
321		1040				1045			1050								
323	cag	gtt	ctc	cgc	gat	ccc	cca	ttt	gcc	agt	ggt	ttg	ccc	gtg	gtg		3204

RAW SEQUENCE LISTING ERROR SUMMARY  
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Input Set : A:\sequence listing.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 3,4,6,7,9,10

Seq#:24; Xaa Pos. 3

Seq#:26; Xaa Pos. 3,4,6,7,9,10

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:26

## VERIFICATION SUMMARY

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L:1140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
L:1410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0  
L:1867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0